

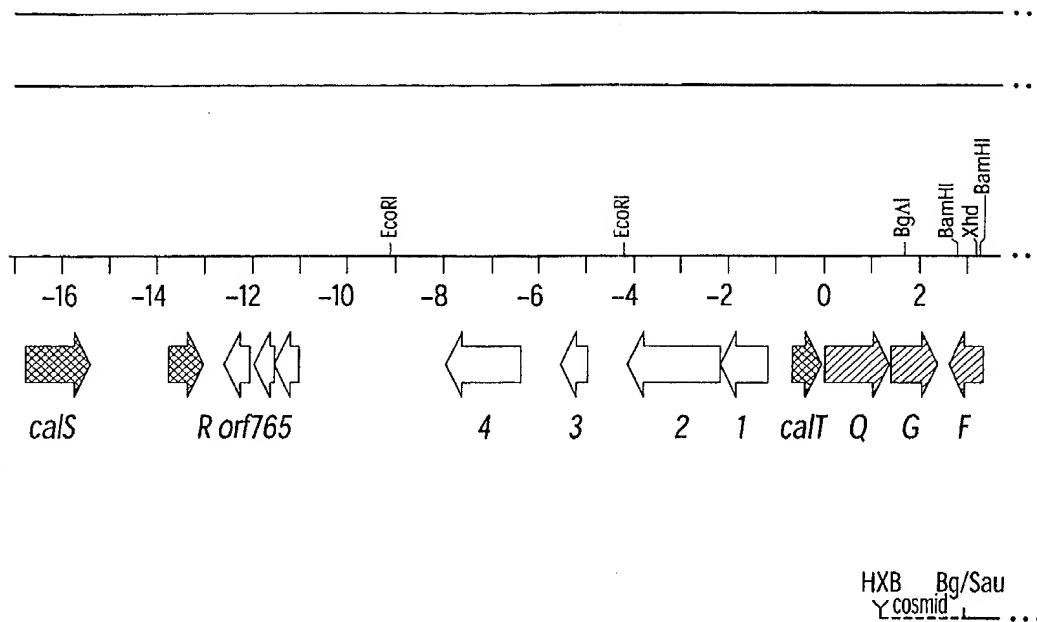
Summary of cosmid clones isolated from <i>M. echinospora</i> genomic library.				
clone <sup>a</sup>	type I PKS genes <sup>b</sup>	type II PKS genes <sup>b</sup>	deoxy sugar genes <sup>b</sup>	resistance ( $\mu\text{g mL}^{-1}$ ) <sup>c</sup>
3a	N.D. <sup>d</sup>	N.D. <sup>d</sup>	N.D. <sup>d</sup>	0.5
4a	N.D. <sup>d</sup>	N.D. <sup>d</sup>	N.D. <sup>d</sup>	0.5
4b	+	+	+	0.5
10a	+	+	+	0.5
13a	+	+	+	0.5
16a	N.D. <sup>d</sup>	N.D. <sup>d</sup>	N.D. <sup>d</sup>	0.5
56	+	+	+	0.1
58	-	-	+	< 0.01
60	+	+	+	0.05
66	-	-	+	0.04
puc18/pBluescript <sup>e</sup>	-	-	-	< 0.01

FIG. 1

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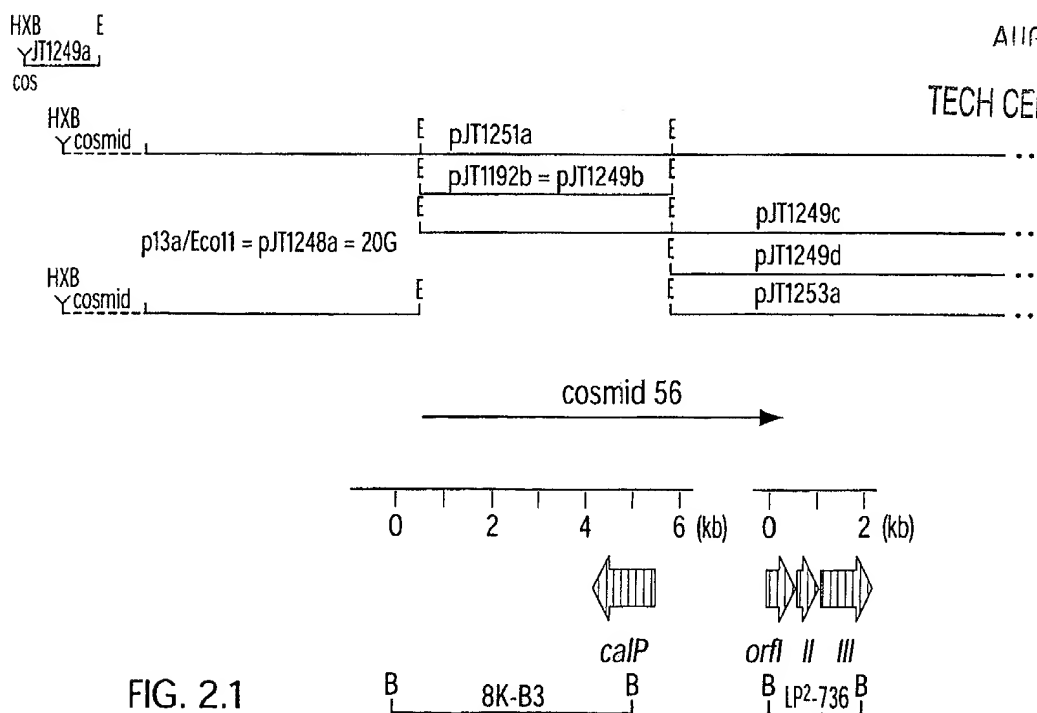


FIG. 2.1

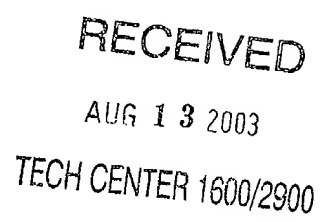
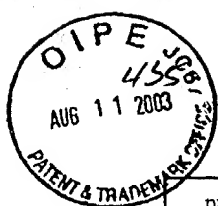


FIG. 2.2



putative polypeptide	number of amino acids	proposed function or sequence similarity detected	probability	start/stop codons	best match
CalA	328	membrane transporter (ATP-binding)	$5.4 \times 10^{-124}$	ATG/TGA	DrrA <sup>97</sup>
CalB	561	membrane transporter	$5.5 \times 10^{-70}$	ATG/TGA	DrrB <sup>97</sup>
CalC	181	calicheamicin resistance protein	confirmed	ATG/TGA	
CalD	263	O-methyltransferase	$1.1 \times 10^{-99}$	ATG/TGA	AveBVII <sup>98</sup>
CalE	420	glycosyltransferase	$4.7 \times 10^{-30}$	GTG/TAG	EryCII <sup>99</sup>
CalF	245	N,N-dimethyltransferase	$1.5 \times 10^{-78}$	ATG/TGA	DesVI <sup>100</sup>
CalG	990	TDP-D-glucose 4,6-dehydratase	confirmed	GTG/TAG	
CalH	338	Perosamine synthetase	confirmed	GTG/TGA	
CalI	568	Dipeptide transporter	$1.7 \times 10^{-24}$	GTG/TGA	DciAE
CalJ	332	O-methyltransferase	$1.0 \times 10^{-37}$	ATG/TGA	DmpM
CalK	440	L-cysteine/cystine C-S-lyase	$1.6 \times 10^{-28}$	GTG/TGA	C-DES
CalL	562	Oligopeptide transporter protein	$9.5 \times 10^{-14}$	ATG/TGA	OppA
CalM	416	Regulatory protein		GTG/TGA	
CalN	398	Glycosyltransferase	$3.4 \times 10^{-79}$	ATG/TGA	Ole1
CalO	331	Hexopyranosyl-2,3-reductase	$4.9 \times 10^{-139}$	ATG/TGA	EryBII
CalP	(179)	Desaturase	$5.7 \times 10^{-7}$	/TGA	CrtI
CalQ	453	UDP-D-glucose 6-dehydrogenase	confirmed	GTG/TGA	
CalR	282	Transcriptional regulator	$6.7 \times 10^{-11}$	ATG/TGA	SC5C7.03
CalS	1113	P <sub>450</sub> oxidase	$2.9 \times 10^{-66}$	GTG/TGA	BioI
CalT	432	oxygenase/halogenase	$2.0 \times 10^{-62}$	GTG/TAA	PCZA361.20
CalU	377	glycosyltransferase	$2.0 \times 10^{-53}$	ATG/TGA	SnogE/D
CalV	125	$\beta$ -keto-acyl synthase III	$2.0 \times 10^{-65}$	ATG/TGA	SC4A9
CalW	(449)	cytochrome P450	$1.0 \times 10^{-91}$	GTG/TGA	CYP105B1
CalX	(197)	TDP-4-keto-6-deoxy-L-hexose 2,3-dehydratase	$1.0 \times 10^{-22}$	/TGA	MtmV
6MSAS	(198)	orsellenic acid synthase	$6.5 \times 10^{-76}$	ATG/	AviM
ActI	(207)	polyketide cyclase	$3.0 \times 10^{-66}$	/TGA	CurF
ActII	136	polyketide cyclase	$5.0 \times 10^{-53}$	ATG/TGA	SchB
ActIII	(308)	polyketide synthase	$8.6 \times 10^{-148}$	GTG/	Pms1
orf1	322	unknown		ATG/TGA	
orf2	654	unknown		ATG/TGA	
orf3	373	integrase	$3.0 \times 10^{-13}$	ATG/TGA	
orf4	521	chromosome partitioning protein	$3.3 \times 10^{-10}$	GTG/TAA	ParA
orf5	175	unknown		ATG/TGA	
orf6	139	unknown		ATG/TGA	
orf7	187	unknown		GTG/TGA	
orf8	266	regulatory protein	$3.0 \times 10^{-66}$	ATG/TGA	KorSA
OrfI	127	hydroxylase	$1.5 \times 10^{-7}$	ATG/TGA	SC4C6.24c
OrfII	248	unknown		GTG/TGA	
OrfIII	298	hydroxylase	$3.3 \times 10^{-90}$	GTG/TGA	SCA32
OrfIV	363	unknown	$5.3 \times 10^{-43}$	GTG/TGA	SC9C7.25
OrfV	288	aminotransferase	$2.9 \times 10^{-37}$	GTG/TGA	SCF55
OrfVI	1012	glu-ammonia-ligase adenyltransferase	exact	GTG/TGA	SCA32
OrfVII	236	Methyltransferase	$8.0 \times 10^{-63}$	GTG/TAG	SCF43A.25c
OrfVIII	441	Integral membrane protein	$8.9 \times 10^{-9}$	GTG/TGA	SCA32
OrfIX	478	Integral membrane protein	$1.1 \times 10^{-21}$	ATG/TGA	MLB268
OrfX	504	Membrane protein	$5.5 \times 10^{-20}$	GTG/TGA	B1496.F1.14
OrfXI	251	Immunity resistance protein	$1.1 \times 10^{-9}$	ATG/TGA	TFXG
IS-element	1209 bp	insertional element	$5.7 \times 10^{-168}$		IS1136 <sup>111</sup>

FIG. 3

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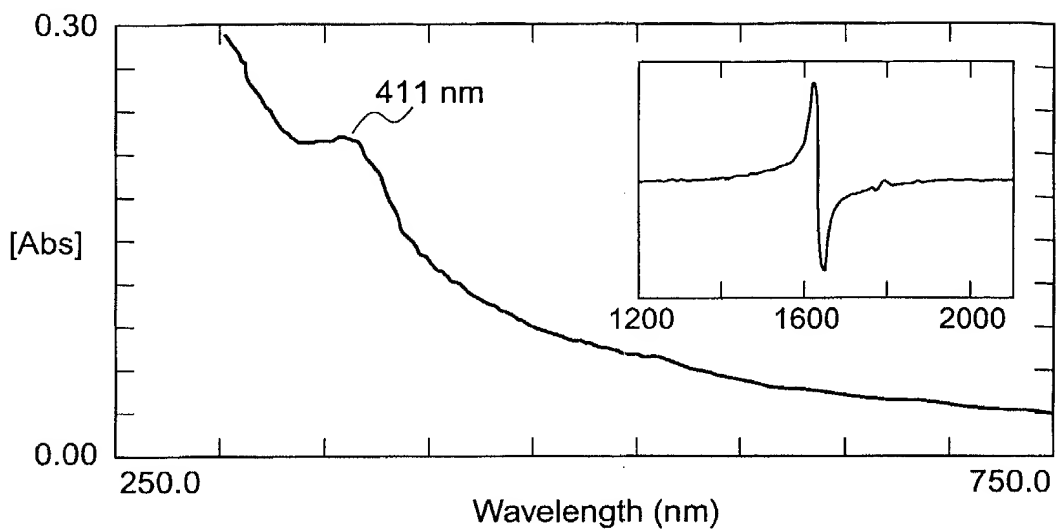


FIG. 4A

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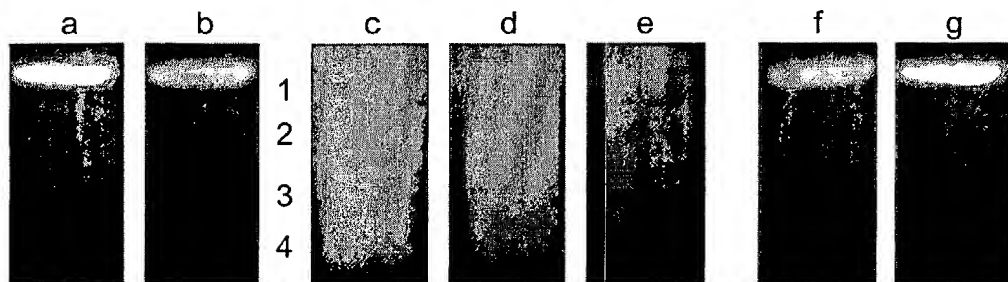


FIG. 4B

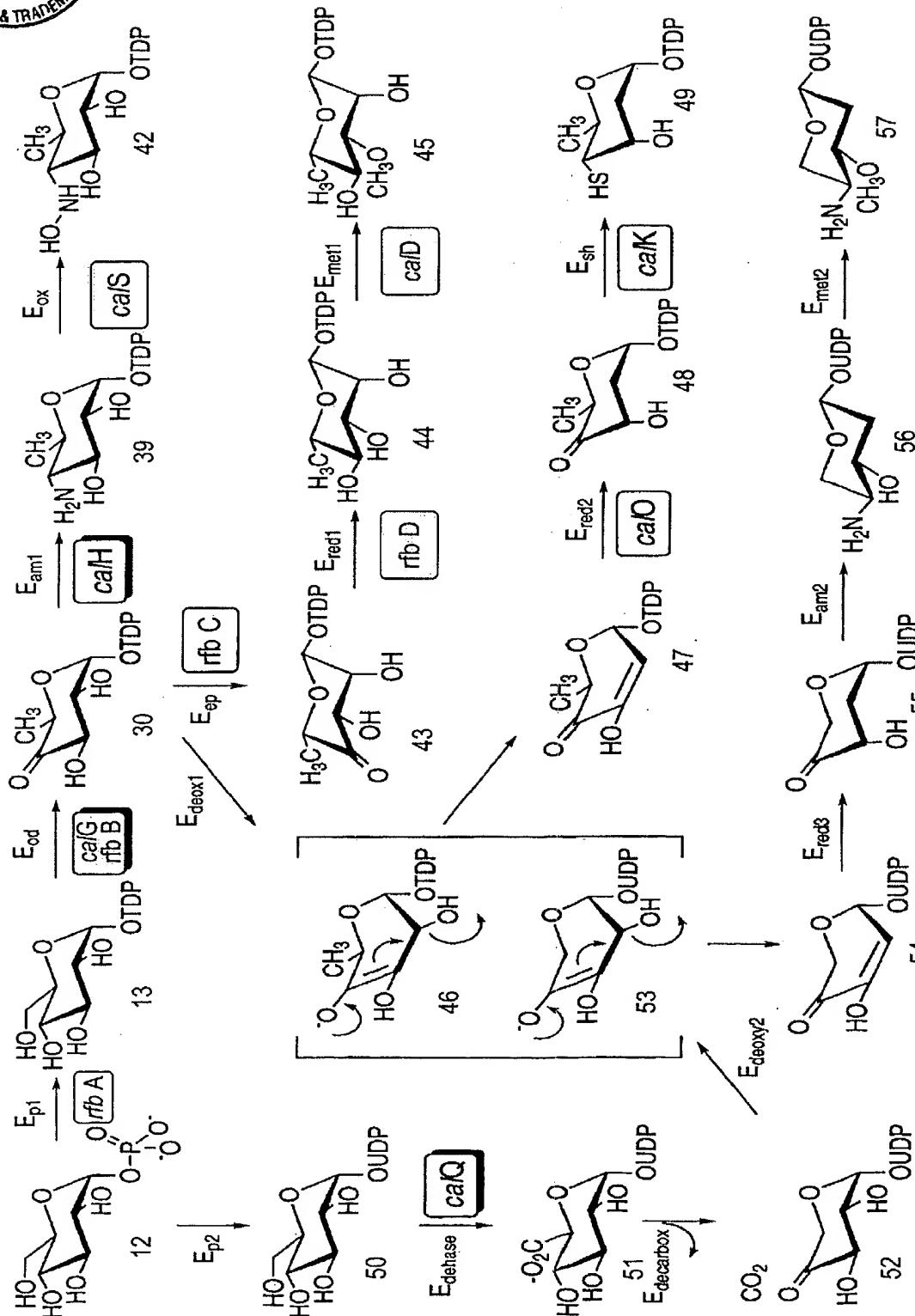


FIG. 5

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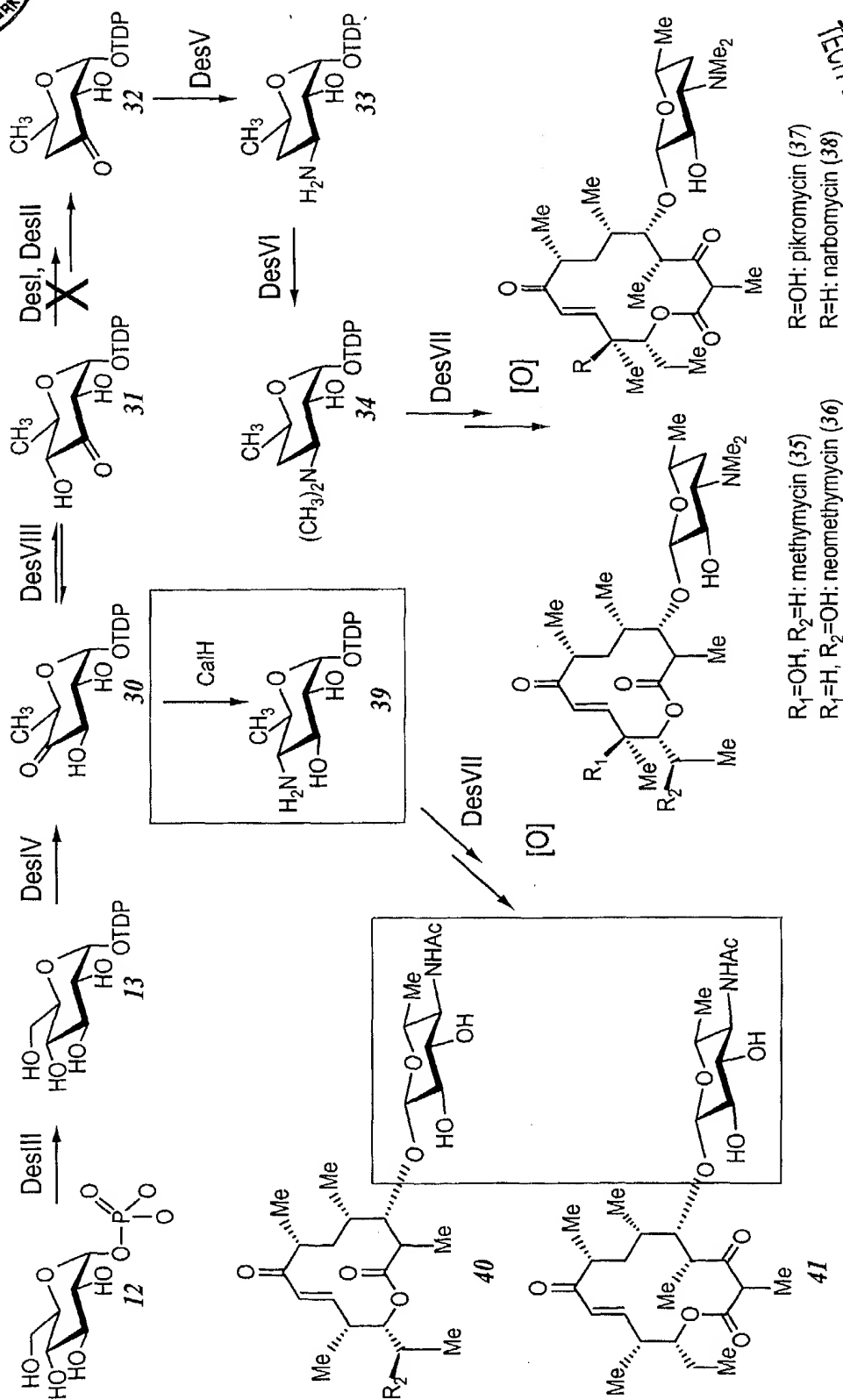


FIG. 6

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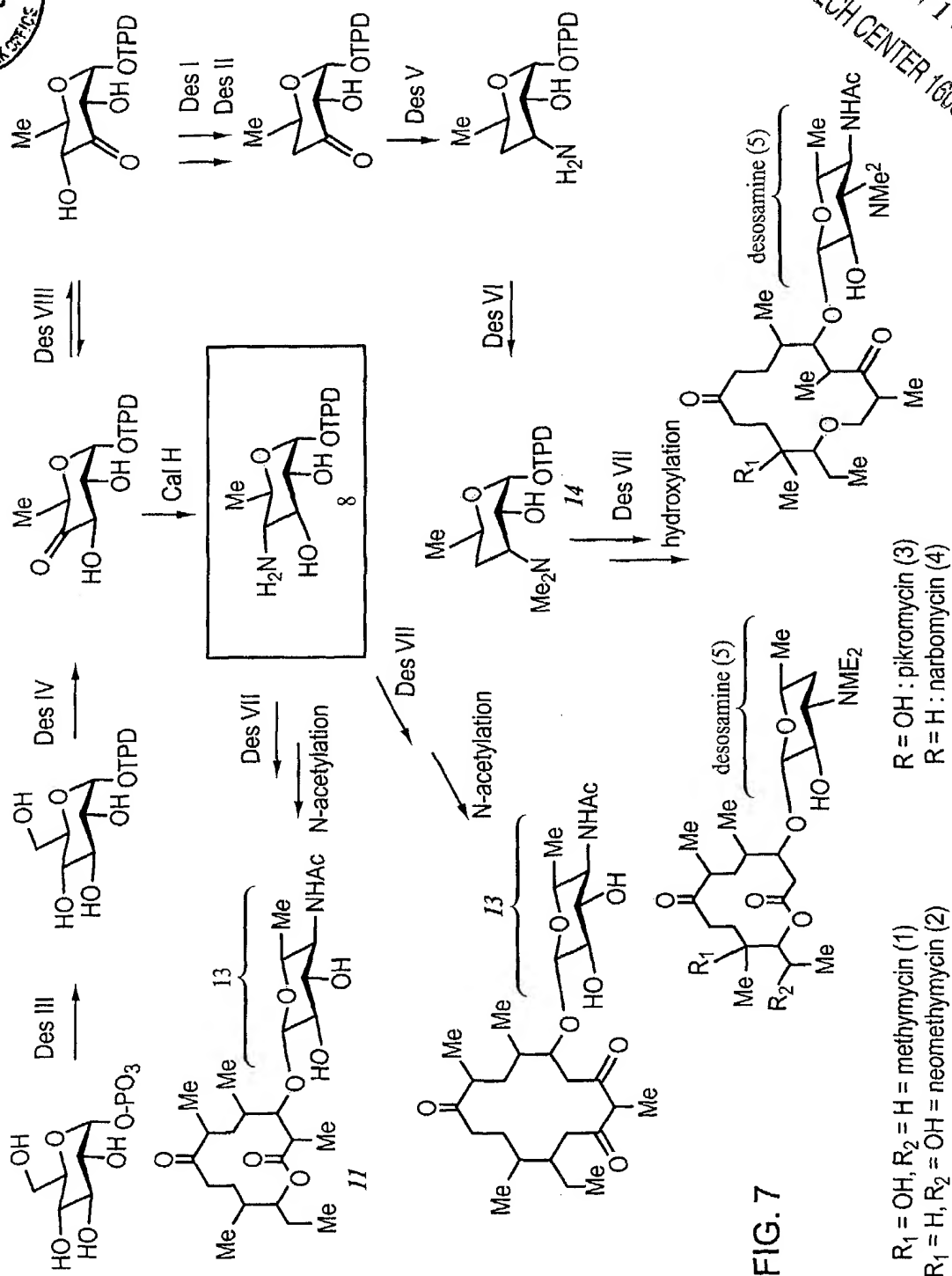


FIG. 7



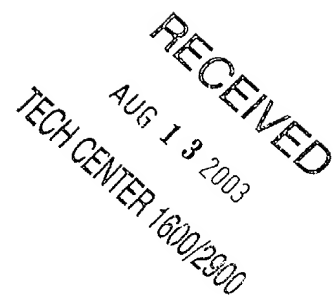
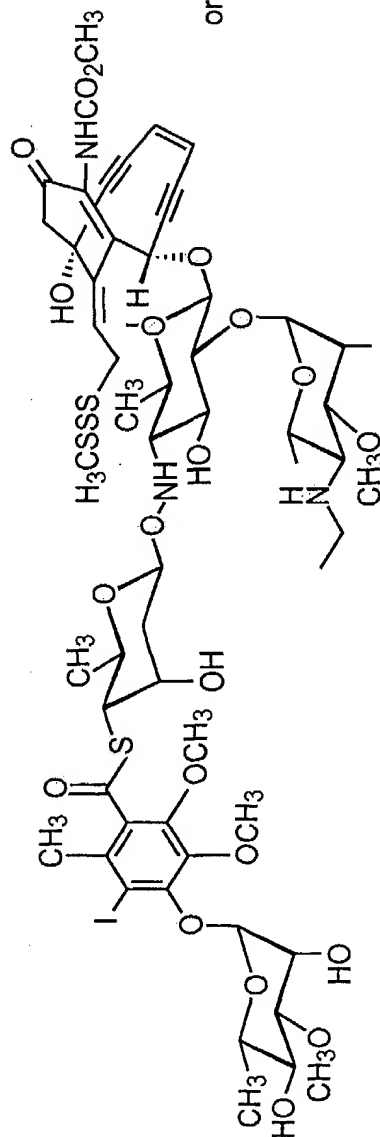
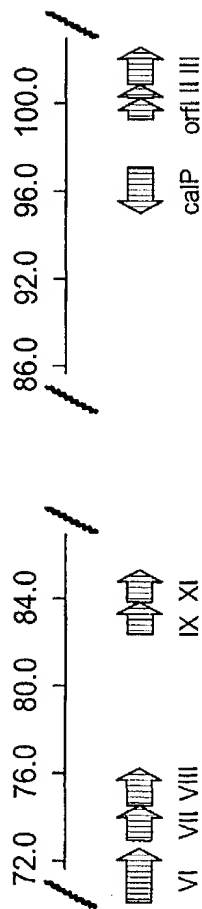
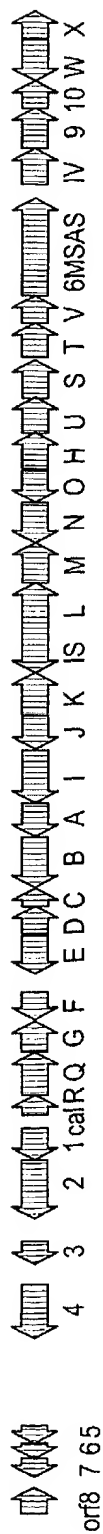
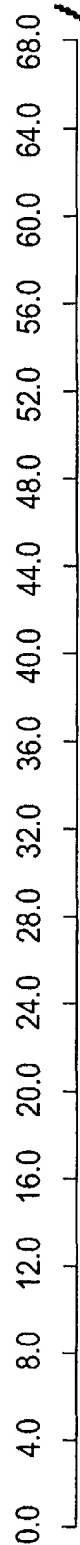


FIG. 8



resistance  
uptake, transport  
glycosyltransferase  
sugar biosynthesis  
regulation  
porcelline acid biosynthesis  
aglycone biosynthesis  
oxidation  
unknown

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**FIG. 9**

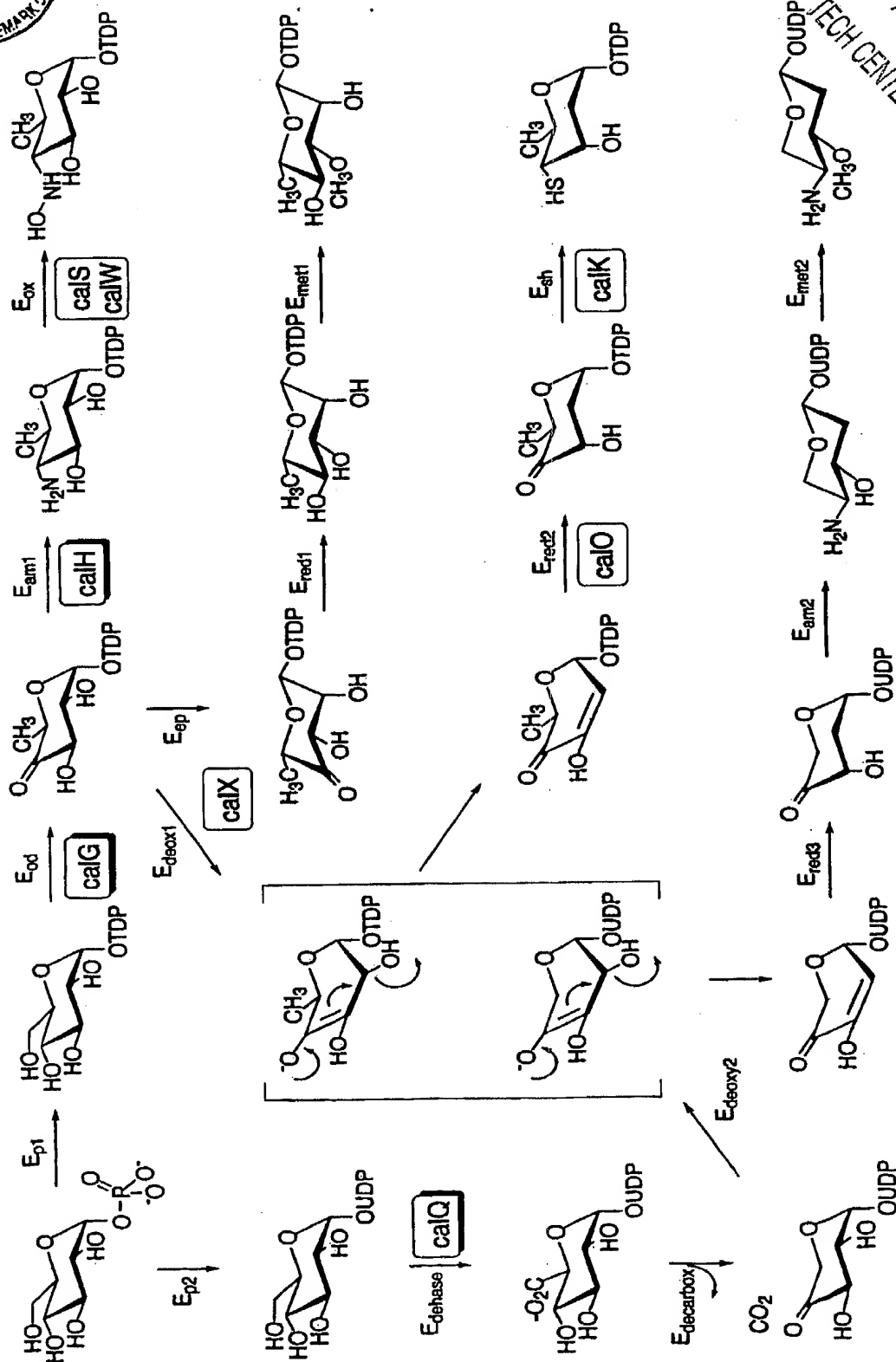
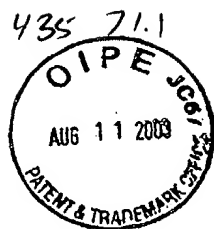
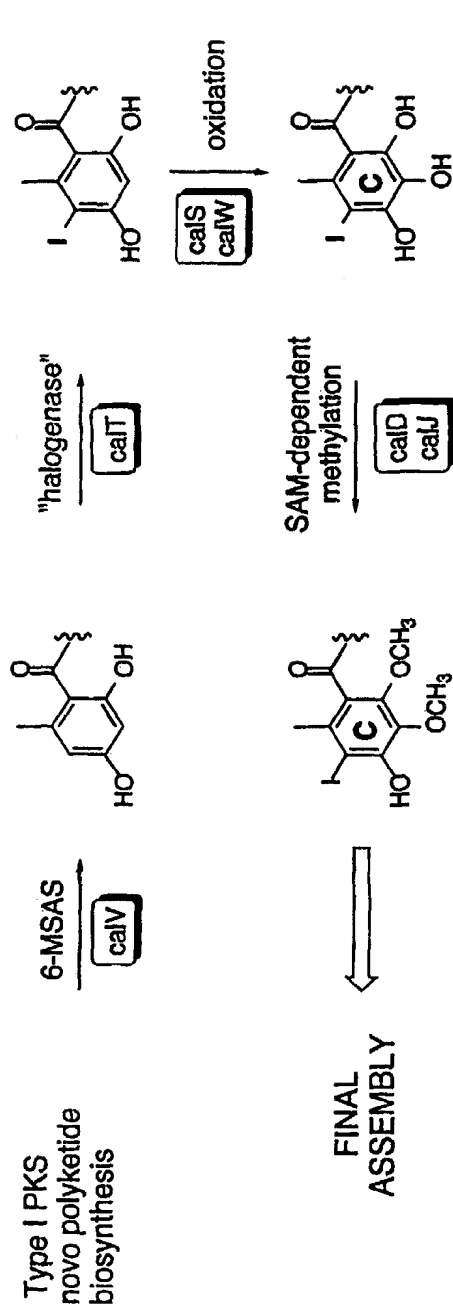


FIG. 10

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The Aryltetracosaccharide Unit (a type I PKS product):



Synthesis of Putative Substrates:

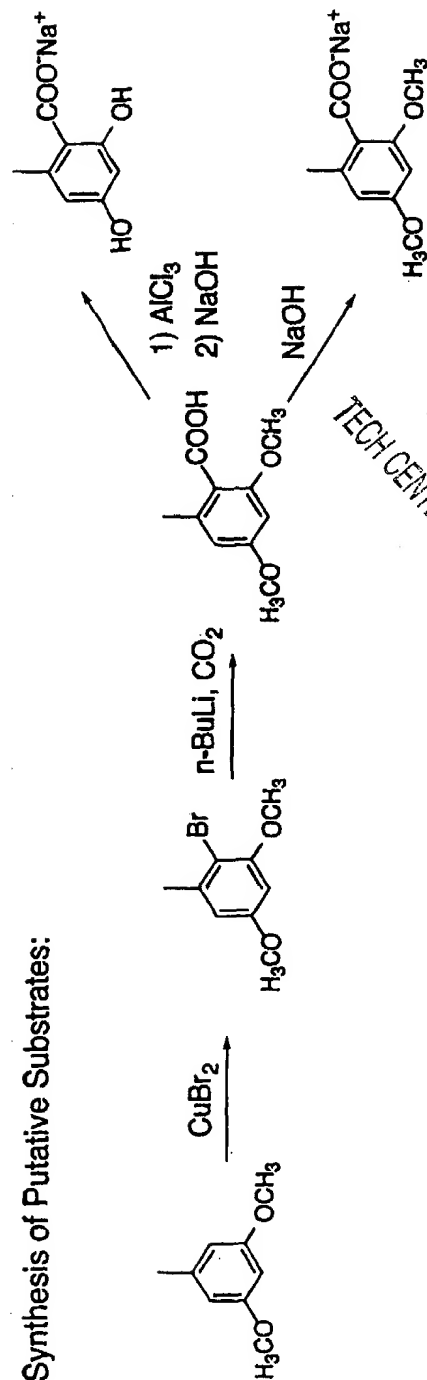


FIG. 11

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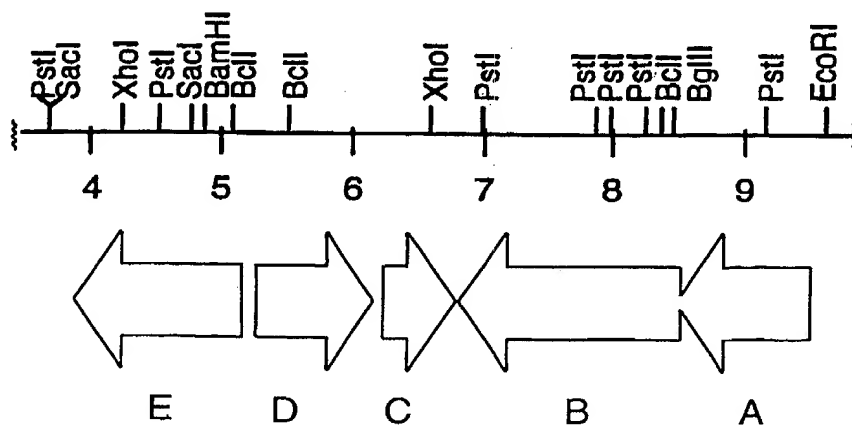
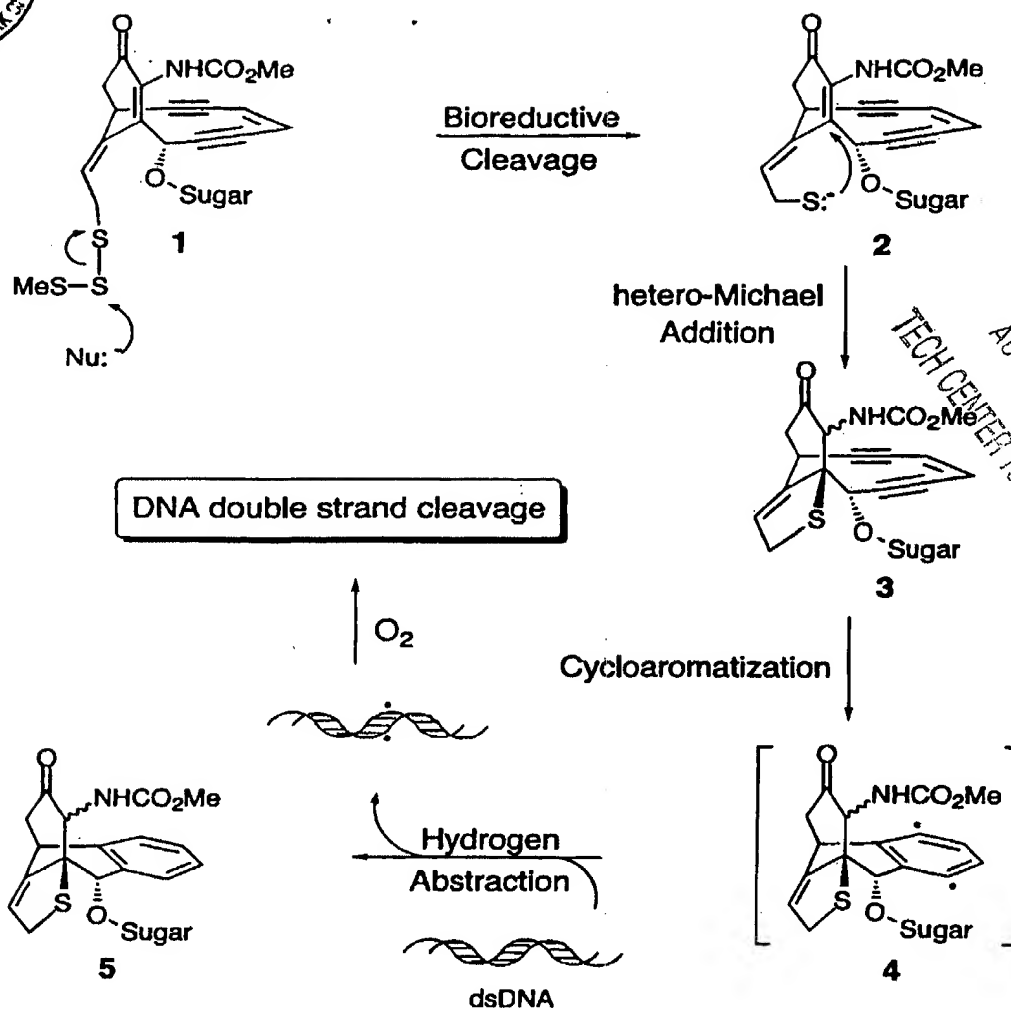
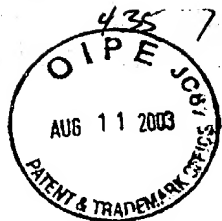


FIG. 12

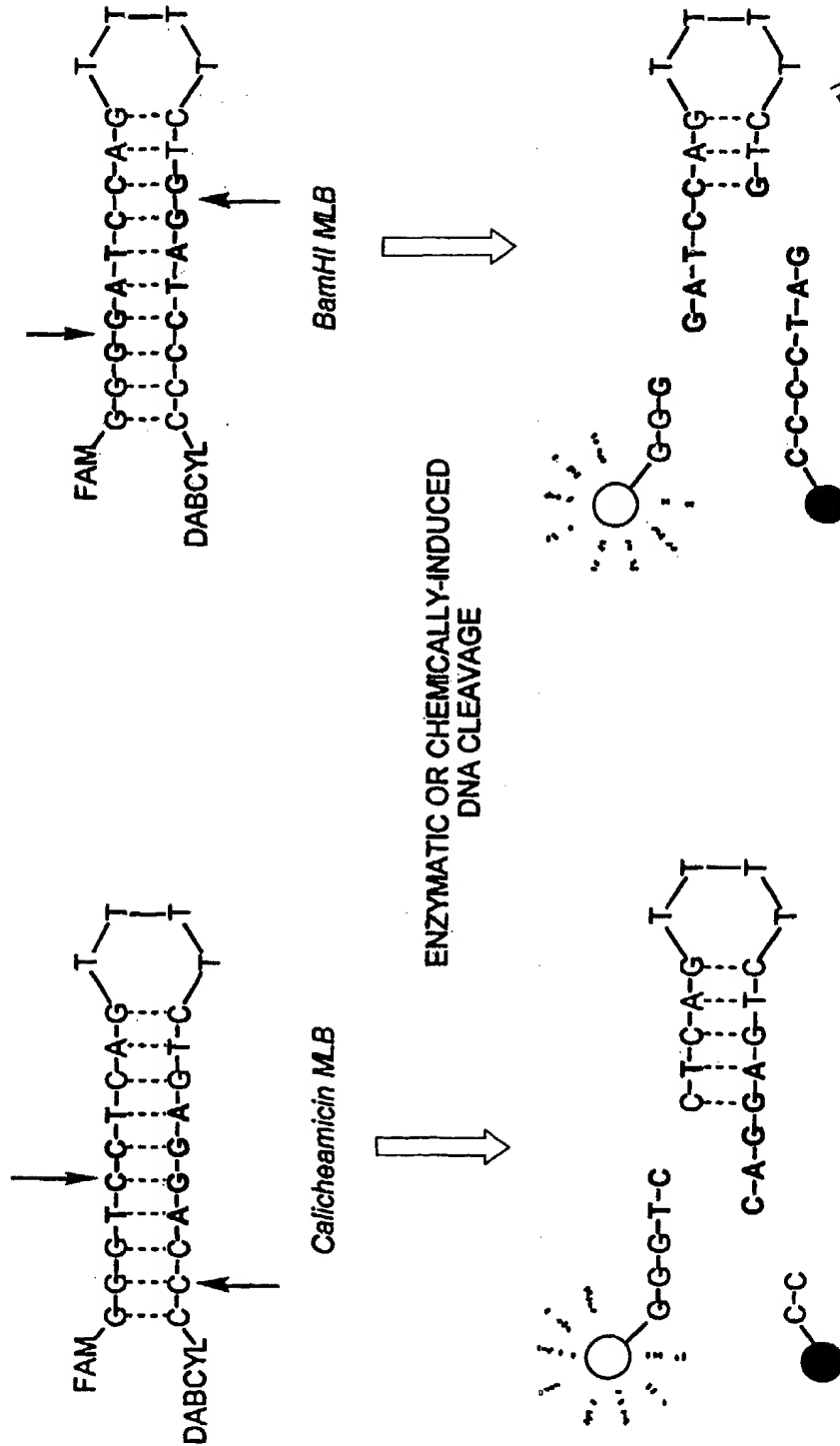


FIG. 13

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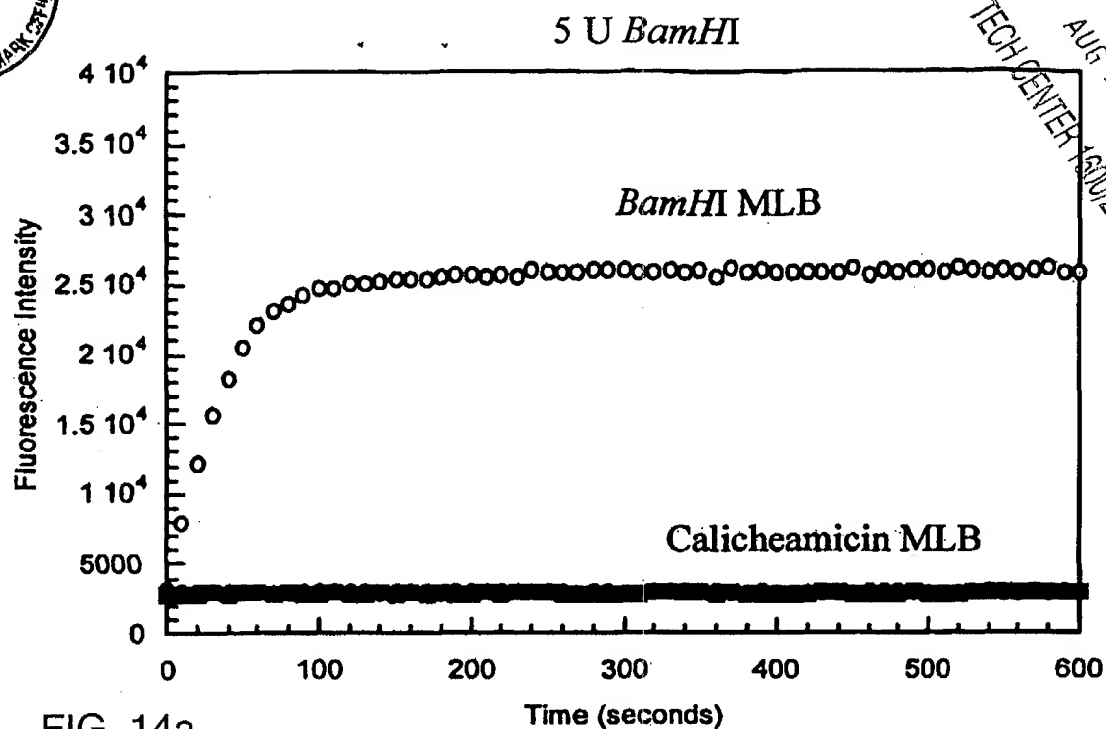


FIG. 14a

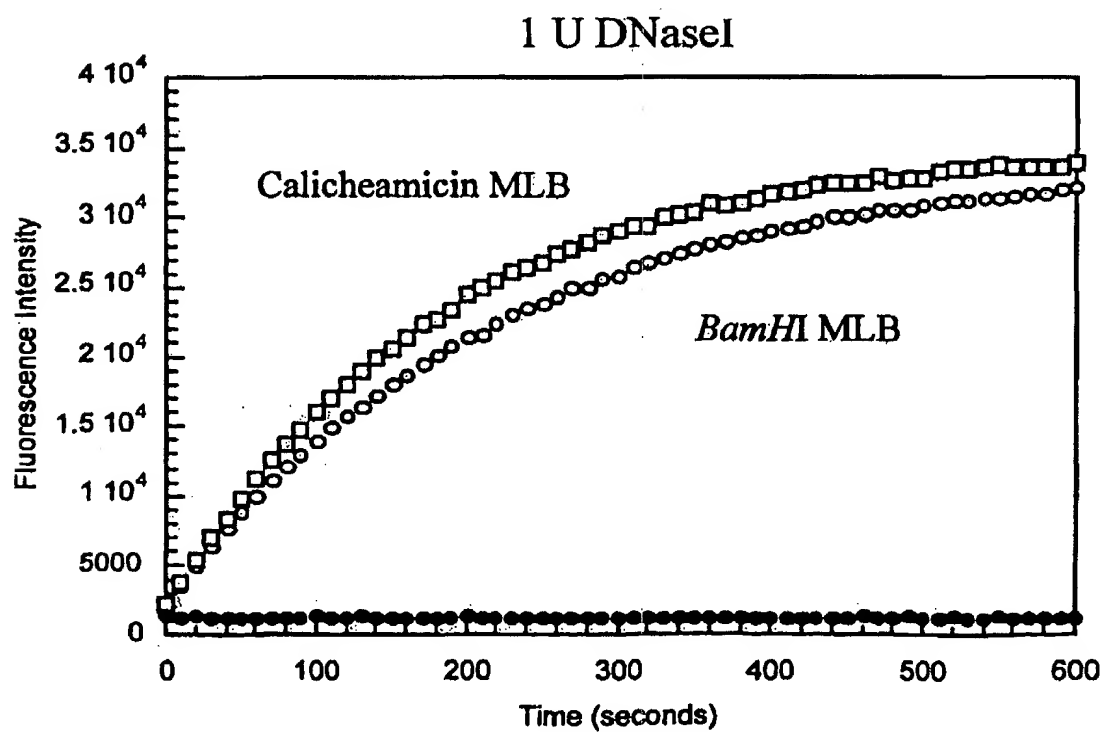


FIG. 14b

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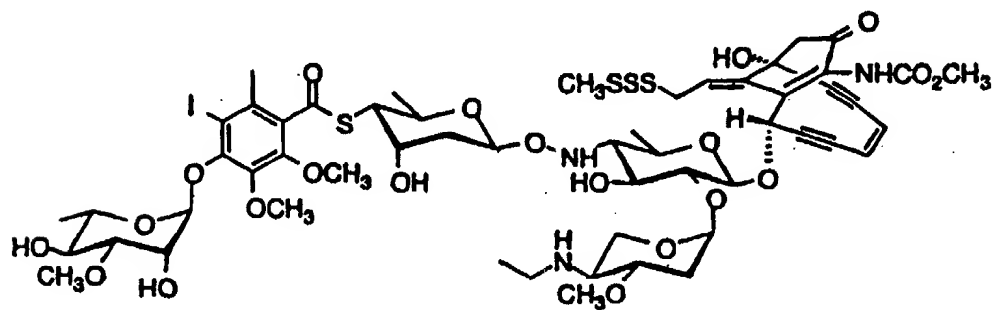
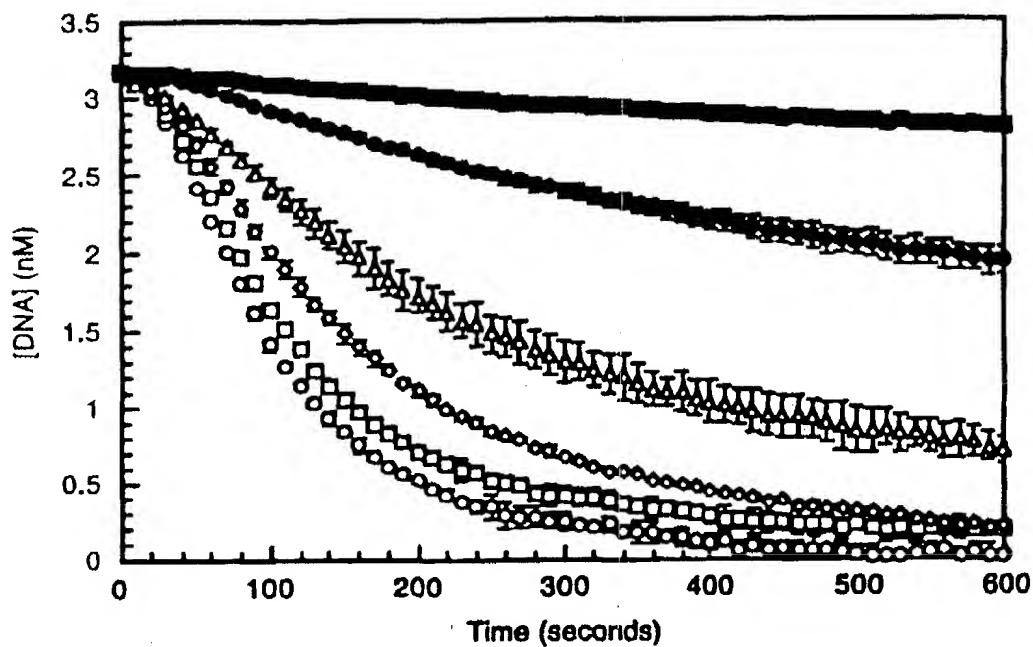
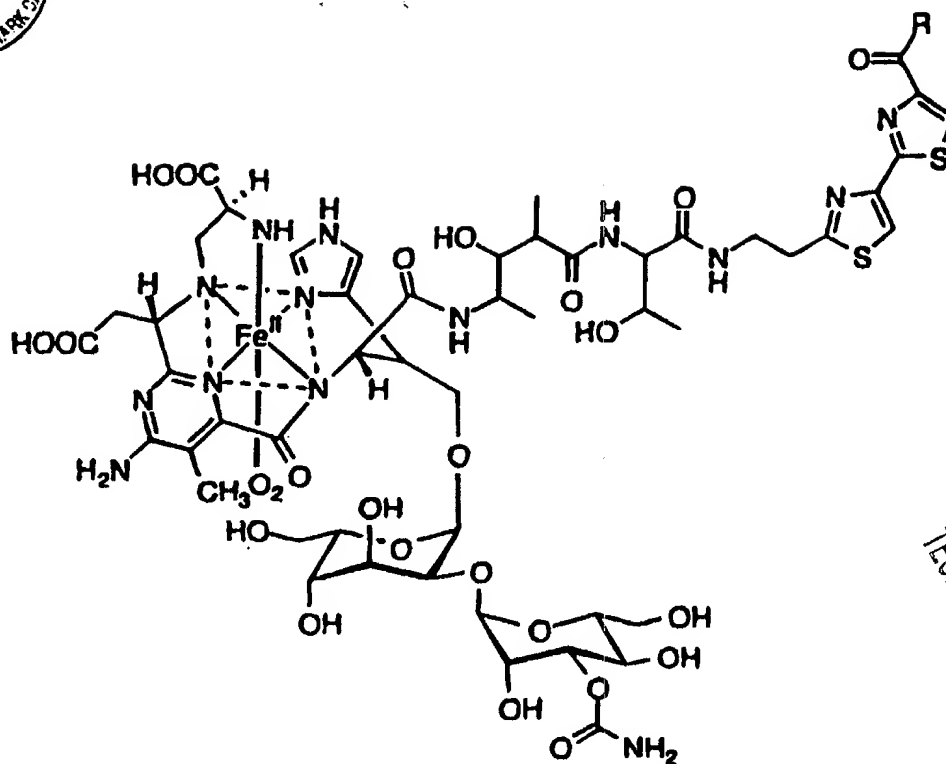


FIG. 15a







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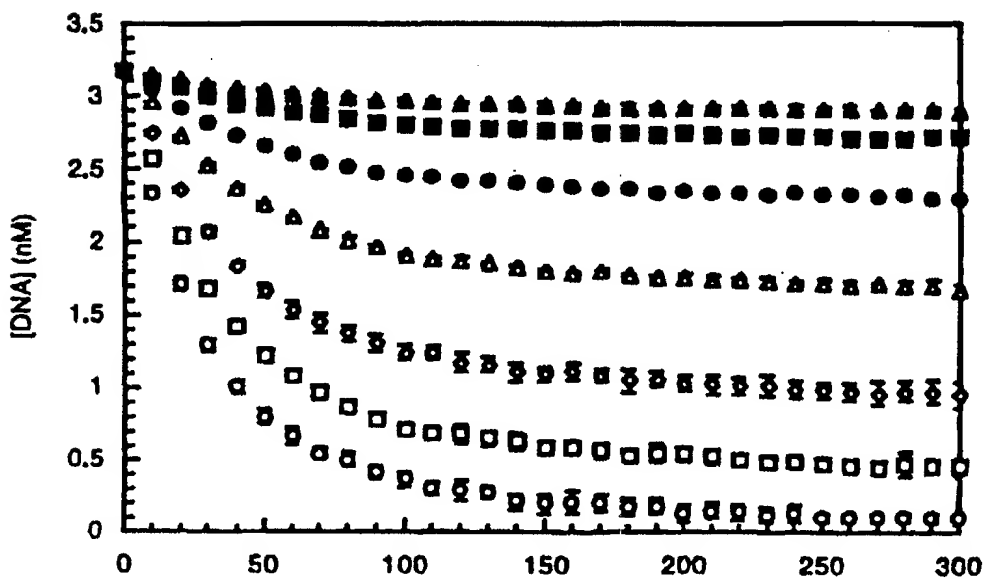
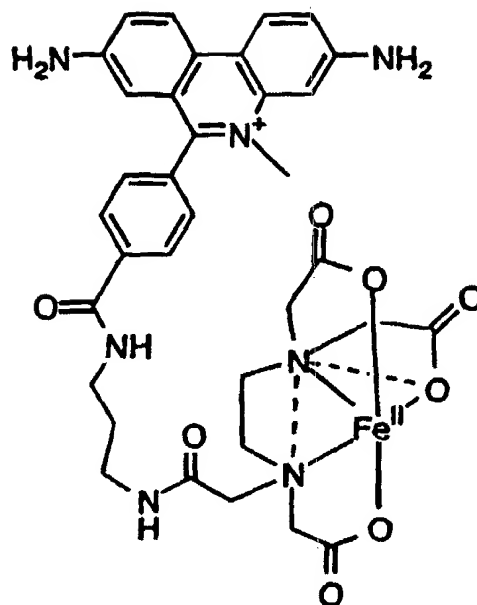
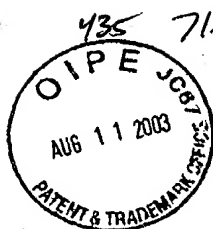


FIG. 16a



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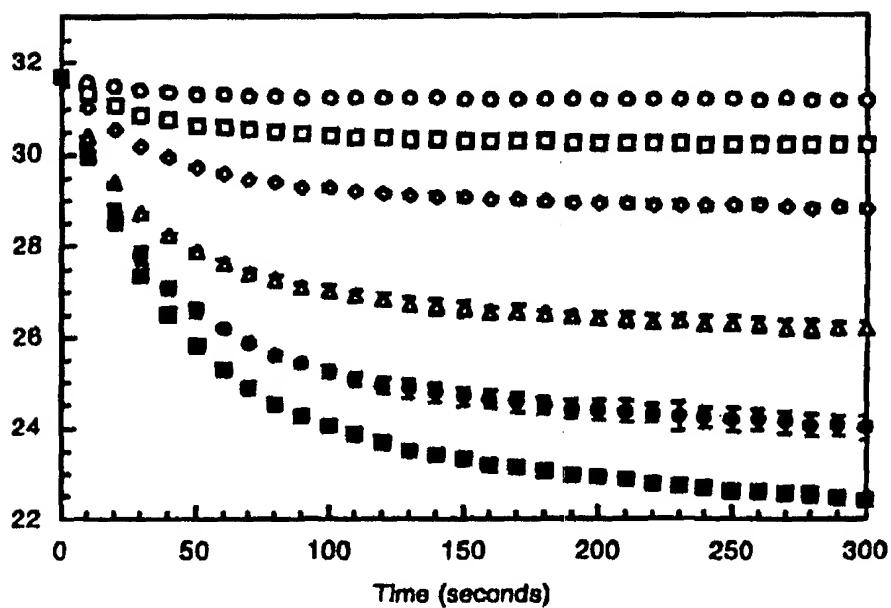
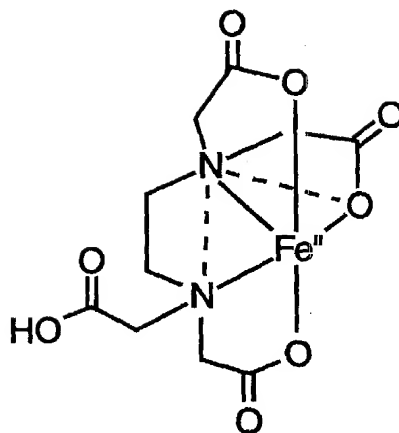


FIG.16c



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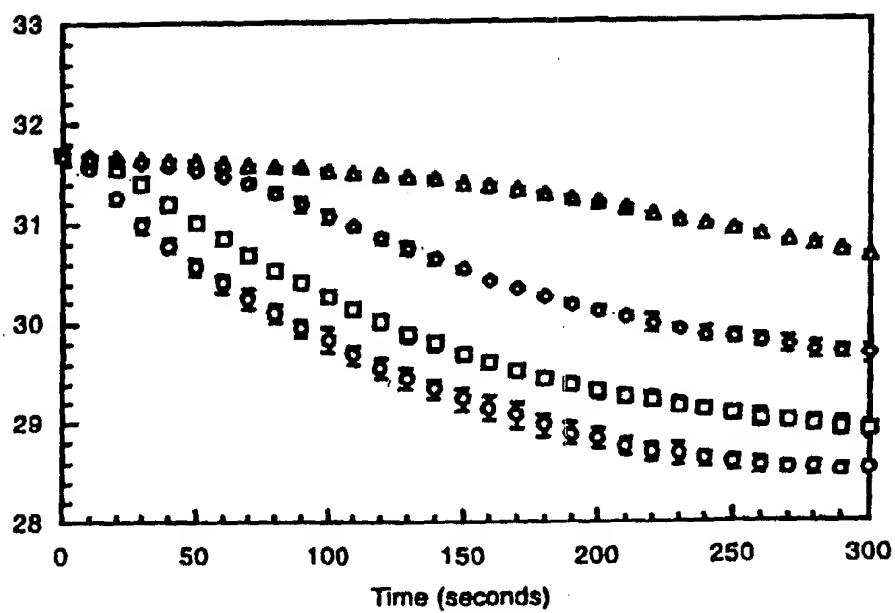


FIG. 16d

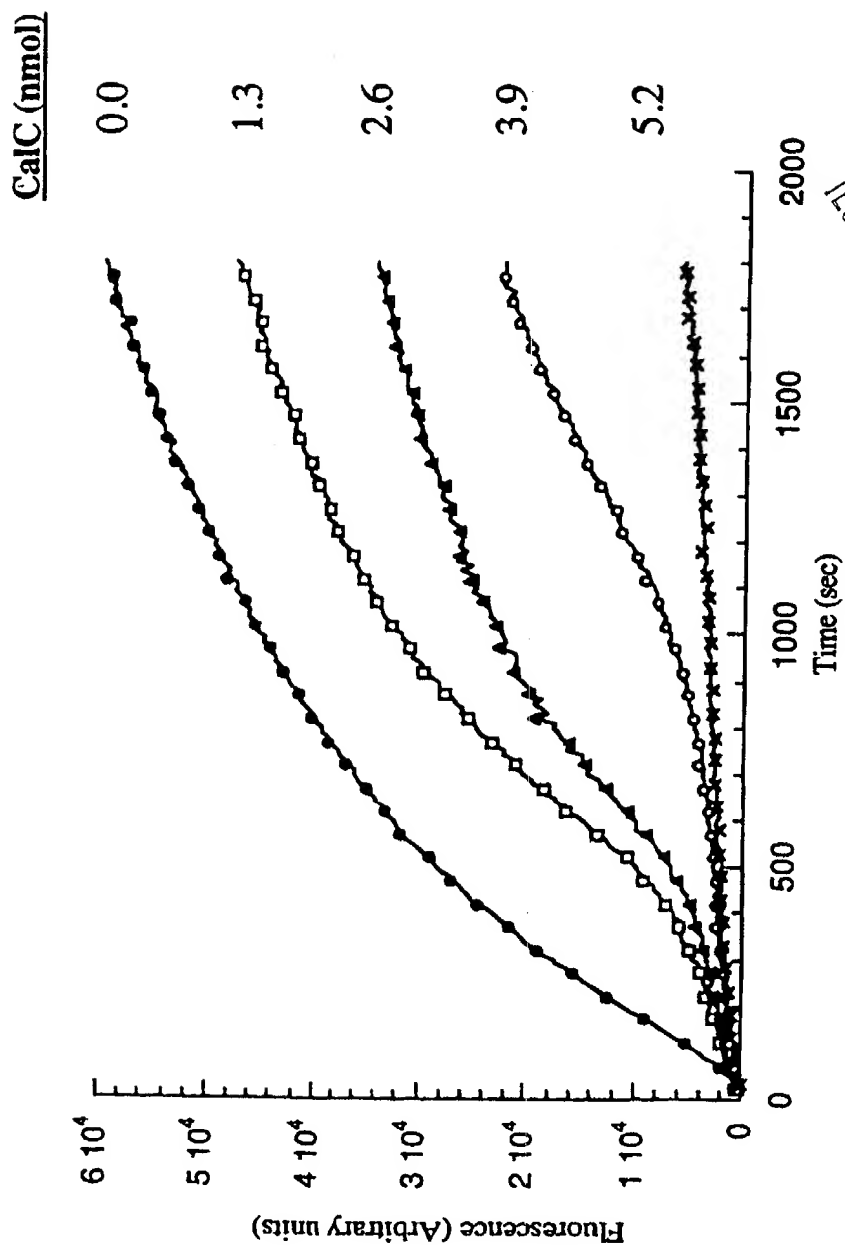


FIG. 17

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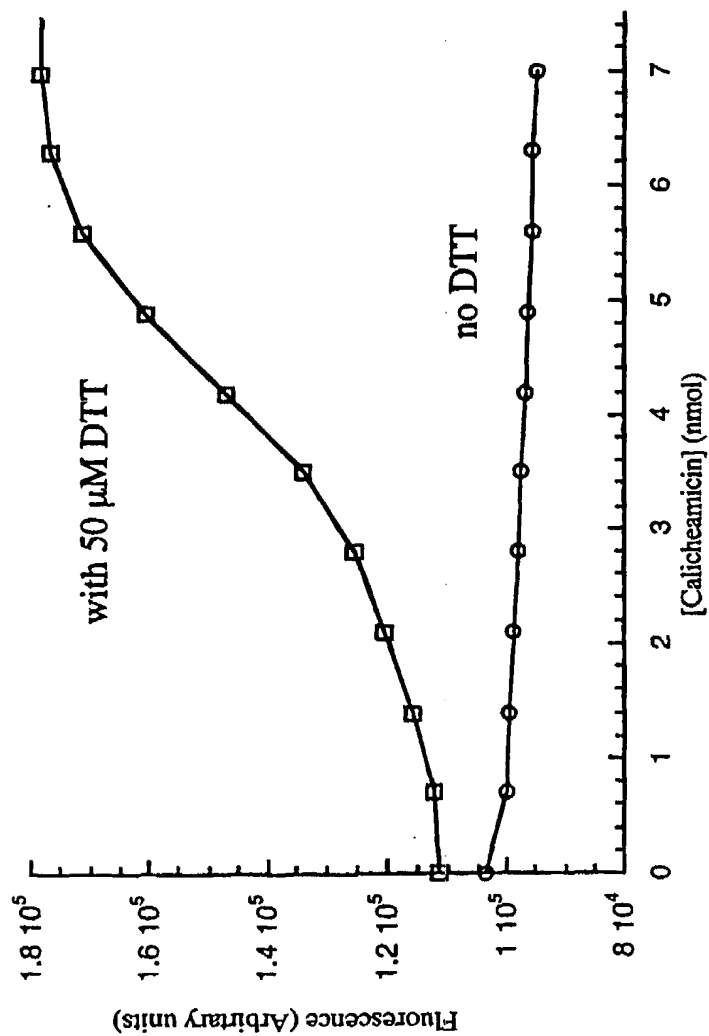
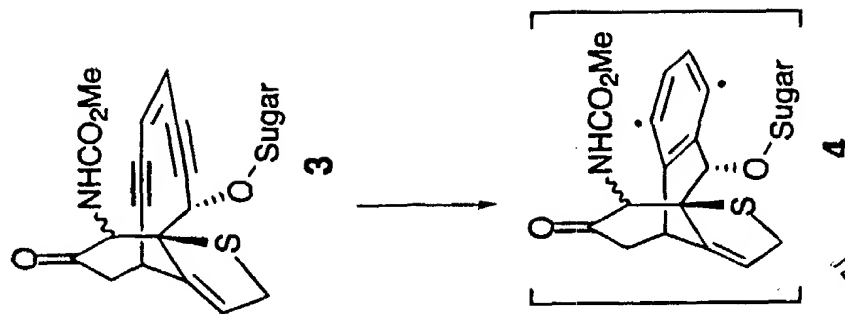


FIG. 18

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